



RECEIVED

OCT 22 2001

TECH CENTER 1600/2900

PATENT

Docket No.: 2283/301

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Leivan DeVeylder et al

Serial No. : 09/574,735

Conf. No. : 1507

Filed : May 18, 2000

For : CYCLIN-DEPENDENT KINASE INHIBITORS
AND USES THEREOF

Examiner:

C. Collins

Art Unit:

1638

STATEMENT UNDER 37 C.F.R. § 1.825(a) AND (b)Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that support for the substitute paper copy of the Sequence Listing exists in the above-captioned application as originally filed. The substitute paper copy of the Sequence Listing submitted herewith does not add new matter to the application as originally filed. In addition, the information recorded in the substitute computer readable form (CRF) of the Sequence Listing submitted herewith, is identical to the information contained in the substitute paper copy of the Sequence Listing.

Respectfully submitted,

Ann R. Pokalsky

Registration No. 34,697

Dated: October 12, 2001

Nixon Peabody LLP
990 Stewart Avenue
Garden City, New York 11530-4838
Telephone: (516) 832-7572
Facsimile: (516) 832-7555
ARP/mm

G201614.1

Certificate of Mailing - 37 CFR 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231, on the date below.

10/12/01
DateMaria Matos
Maria Matos

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

RECEIVED

OCT 22 2001

Applicant Must Provide:

TECH CENTER 1600/2900

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

#19



RECEIVED

OCT 22 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> De Veylder, Lieven
Beeckman, Tom
Inzé, Dirk
Van Camp, Wim
Krols, Luc

<120> Cyclin-dependent kinase inhibitors and uses thereof

<130> 2283/301

<140> US 09/574,735

<141> 2000-05-18

<160> 48

<170> PatentIn version 3.0

<210> 1

<211> 932

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (86)..(712)

<400> 1

```

ggcacgagga gaaccacaaa cacgcacaca taacgagtga ttttagagag agatagagat      60
ctggaaggtg acgtcgtagg agatt atg gcg gcg gtt agg aga aga gaa cga      112
                               Met Ala Ala Val Arg Arg Arg Glu Arg
                               1                               5
gat gtg gtt gaa gag aat gga gtt acg acg acg acg gtg aaa cga agg      160
Asp Val Val Glu Glu Asn Gly Val Thr Thr Thr Thr Val Lys Arg Arg
10                               15                               20                               25
aag atg gag gag gaa gtg gat tta gtg gaa tct agg ata att ctg tct      208
Lys Met Glu Glu Glu Val Asp Leu Val Glu Ser Arg Ile Ile Leu Ser
                               30                               35                               40
ccg tgt gta cag gcg acg aat cgc ggt gga att gtg gcg aga aat tca      256
Pro Cys Val Gln Ala Thr Asn Arg Gly Gly Ile Val Ala Arg Asn Ser
                               45                               50                               55
gca gga gcg tcg gag acg agt gtt gtt ata gta cga cgg cga gat tct      304
Ala Gly Ala Ser Glu Thr Ser Val Val Ile Val Arg Arg Arg Asp Ser
                               60                               65                               70
cct ccg gtt gaa gaa cag tgt caa atc gaa gaa gaa gat tcg tcg gtt      352
Pro Pro Val Glu Glu Gln Cys Gln Ile Glu Glu Glu Asp Ser Ser Val
75                               80                               85
tcg tgt tgt tct aca tcg gaa gag aaa tcg aaa cgg aga atc gaa ttt      400
Ser Cys Cys Ser Thr Ser Glu Glu Lys Ser Lys Arg Arg Ile Glu Phe
90                               95                               100                               105
gta gat ctt gag gaa aat aac ggt gac gat cgt gaa aca gaa acg tcg      448
Val Asp Leu Glu Glu Asn Asn Gly Asp Asp Arg Glu Thr Glu Thr Ser
                               110                               115                               120

```

[illegible]

```
<210> 2
<211> 209
<212> PRT
<213> Arabidopsis thaliana
```

[illegible]

<210> 3
 <211> 875
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (11)..(658)

<400> 3
 ggcacgagag aaa tca aag ata act ggc gat atc agc gtc atg gaa gtc 49
 Lys Ser Lys Ile Thr Gly Asp Ile Ser Val Met Glu Val
 1 5 10
 tct aaa gca aca gct cca agt cca ggt gtt cga acc aga gcc gct aaa 97
 Ser Lys Ala Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys
 15 20 25
 acc cta gcc ttg aag cgg ctt aat tcc tcc gcc gct gat tca gct cta 145
 Thr Leu Ala Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu
 30 35 40 45
 cct aac gac tct tct tgc tat ctt cag ctc cgt agc cgc cgt ctc gag 193
 Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu
 50 55 60
 aaa ccc tct tcg ctg att gaa ccg aaa cag ccg ccg aga gtt cac aga 241
 Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg
 65 70 75
 tcg gga att aaa gag tct ggt tcc agg tct cgc gtt gac tcg gtt aac 289
 Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn
 80 85 90
 tcg gtt cct gta gct cag agc tct aat gaa gat gaa tgt ttt gac aat 337
 Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn
 95 100 105
 ttc gtg agt gtc caa gtt tct tgt ggt gaa aac agt ctc ggt ttt gaa 385
 Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu
 110 115 120 125
 tca aga cac agc aca agg gag agc acg cct tgt aac ttt gtt gag gat 433
 Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp
 130 135 140
 atg gag atc atg gtt aca cca ggg tct agc acg agg tcg atg tgc aga 481
 Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg
 145 150 155
 gca acc aaa gag tac aca agg gaa caa gat aac gtg atc ccg acc act 529
 Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr
 160 165 170
 agt gaa atg gag gag ttc ttt gca tat gca gag cag cag caa cag agg 577
 Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Gln Arg
 175 180 185
 cta ttc atg gag aag tac aac ttc gac att gtg aat gat atc ccc ctc 625
 Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu
 190 195 200 205
 agc gga cgt tac gaa tgg gtg caa gtc aaa cca tgaagttcaa aaggaaacag 678
 Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
 210 215
 ctccaaaaga catggtgtga agttagagaa tgtgatggag ttaacagact aaccaaacat 738
 cagaaatcgt gtaatcttaa gtaataatgt ggtagagaa caagtttgag agtagcttag 798
 ggaccttaaa acctcacacc atttgtaata ctaatcttct tcagatgctt agtgaaattt 858
 tctcatctgt ttctttc 875

<210> 4
 <211> 222
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
 Met Gly Lys Tyr Met Lys Lys Ser Lys Ile Thr Gly Asp Ile Ser Val
 1 5 10 15
 Met Glu Val Ser Lys Ala Thr Ala Pro Ser Pro Gly Val Arg Thr Arg
 20 25 30
 Ala Ala Lys Thr Leu Ala Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp
 35 40 45
 Ser Ala Leu Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg
 50 55 60
 Arg Leu Glu Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg
 65 70 75 80
 Val His Arg Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp
 85 90 95
 Ser Val Asn Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys
 100 105 110
 Phe Asp Asn Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu
 115 120 125
 Gly Phe Glu Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe
 130 135 140
 Val Glu Asp Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser
 145 150 155 160
 Met Cys Arg Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile
 165 170 175
 Pro Thr Thr Ser Glu Met Glu Glu Phe Ala Tyr Ala Glu Gln Gln
 180 185 190
 Gln Gln Arg Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp
 195 200 205
 Ile Pro Leu Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
 210 215 220

<210> 5
 <211> 1193
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (92)..(763)

<400> 5
 aaaccactct tcaaatcaaa cactttctta cataagattc ctctgttttt ctgtgtgctt 60
 cttcaaattc ttccctgtt tttcaacttc a atg ggg aag tac atg aag aaa 112
 Met Gly Lys Tyr Met Lys Lys
 1 5
 ctc aaa tcc aaa tca gaa tct cct tca ccc aat tca aca cca aca cca 160
 Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
 10 15 20
 tca cca tca cca tca cca aca cca atc acc acc aat tca cca cca cca 208
 Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
 25 30 35
 aca aca ccc aat tcc tct gat ggt gtt cga act cgt gct aga acc cta 256
 Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
 40 45 50 55
 gct ttg gag aat tcc aac aat cag aat cag aat ctt tct gtt tct tct 304

Ala	Leu	Glu	Asn	Ser	Asn	Asn	Gln	Asn	Gln	Asn	Leu	Ser	Val	Ser	Ser		
			60						65					70			
gat	tct	tac	ctt	cag	ctg	agg	aac	cgt	cgc	ctt	aag	aga	ccc	cta	att		352
Asp	Ser	Tyr	Leu	Gln	Leu	Arg	Asn	Arg	Arg	Leu	Lys	Arg	Pro	Leu	Ile		
			75					80					85				
agg	caa	cat	tcc	gct	aag	agg	aat	aag	ggg	cat	gat	gga	aac	cct	aaa		400
Arg	Gln	His	Ser	Ala	Lys	Arg	Asn	Lys	Gly	His	Asp	Gly	Asn	Pro	Lys		
		90					95				100						
tcc	cca	att	ggg	gat	tca	att	gct	gaa	gag	aaa	act	ggt	cag	aag	agt		448
Ser	Pro	Ile	Gly	Asp	Ser	Ile	Ala	Glu	Glu	Lys	Thr	Val	Gln	Lys	Ser		
	105					110					115						
cct	gag	cct	gaa	aat	gct	gaa	ttc	aag	gag	aat	gct	gag	gat	act	gag		496
Pro	Glu	Pro	Glu	Asn	Ala	Glu	Phe	Lys	Glu	Asn	Ala	Glu	Asp	Thr	Glu		
120				125						130					135		
aga	agc	gct	agg	gaa	act	aca	ccc	gtc	cat	ttg	ata	atg	cga	gca	gac		544
Arg	Ser	Ala	Arg	Glu	Thr	Thr	Pro	Val	His	Leu	Ile	Met	Arg	Ala	Asp		
			140					145					150				
ggt	ctc	agg	cct	cct	agg	cca	att	acc	agg	cgt	act	ttt	cca	act	gaa		592
Val	Leu	Arg	Pro	Pro	Arg	Pro	Ile	Thr	Arg	Arg	Thr	Phe	Pro	Thr	Glu		
			155					160					165				
gct	aat	ccc	aaa	acg	gag	cag	cca	act	atc	cca	att	tca	cgc	gaa	ttt		640
Ala	Asn	Pro	Lys	Thr	Glu	Gln	Pro	Thr	Ile	Pro	Ile	Ser	Arg	Glu	Phe		
		170					175					180					
gag	gaa	ttc	tgt	gct	aaa	cat	gaa	gcc	gag	cag	caa	agg	gag	ttc	atg		688
Glu	Glu	Phe	Cys	Ala	Lys	His	Glu	Ala	Glu	Gln	Gln	Arg	Glu	Phe	Met		
	185				190					195							
gag	aag	tac	aac	ttt	gat	cct	gtg	aca	gag	cag	cca	ctc	cca	ggg	cgt		736
Glu	Lys	Tyr	Asn	Phe	Asp	Pro	Val	Thr	Glu	Gln	Pro	Leu	Pro	Gly	Arg		
200				205					210					215			
tac	gaa	tg	gaa	aaa	gtg	tcg	ccc	tag	aaggcaggct	agtattaagt							783
Tyr	Glu	Trp	Glu	Lys	Val	Ser	Pro										
			220														
gttccatcaa	tacatcttta	aagtagcagc	agggttagaa	tttgttgaaa	agggtggtgg												843
tgctatttcc	attttccatc	actttctatt	tacttgtaaa	gaaagtagga	ctttcaacat												903
atgtagacta	atgatctgta	actttacaga	ggtgttgatt	acacaacaat	acaaagtcct												963
ttgtctagca	gatcattaaa	gaagggtttg	agggaataag	ggtctctagt	tgtagggttt												1023
agggtataaa	atcaaagtag	ggtatgtaag	agagggttta	caagaatttc	cttttggtct												1083
tggtgtttac	tcttggtttg	tctatacttg	tactcatgga	acttcaacaa	actcttaaga												1143
aataaagaac	cagatctccc	tcaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa													1193

<210> 6
 <211> 223
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
 Met Gly Lys Tyr Met Lys Lys Leu Lys Ser Lys Ser Glu Ser Pro Ser
 1 5 10 15
 Pro Asn Ser Thr Pro Thr Pro Ser Pro Ser Pro Ser Pro Thr Pro Ile
 20 25 30
 Thr Thr Asn Ser Pro Pro Pro Thr Thr Pro Asn Ser Ser Asp Gly Val
 35 40 45
 Arg Thr Arg Ala Arg Thr Leu Ala Leu Glu Asn Ser Asn Asn Gln Asn
 50 55 60
 Gln Asn Leu Ser Val Ser Ser Asp Ser Tyr Leu Gln Leu Arg Asn Arg
 65 70 75 80
 Arg Leu Lys Arg Pro Leu Ile Arg Gln His Ser Ala Lys Arg Asn Lys
 85 90 95
 Gly His Asp Gly Asn Pro Lys Ser Pro Ile Gly Asp Ser Ile Ala Glu
 100 105 110

Glu	Lys	Thr	Val	Gln	Lys	Ser	Pro	Glu	Pro	Glu	Asn	Ala	Glu	Phe	Lys
			115				120					125			
Glu	Asn	Ala	Glu	Asp	Thr	Glu	Arg	Ser	Ala	Arg	Glu	Thr	Thr	Pro	Val
	130					135					140				
His	Leu	Ile	Met	Arg	Ala	Asp	Val	Leu	Arg	Pro	Pro	Arg	Pro	Ile	Thr
145					150					155				160	
Arg	Arg	Thr	Phe	Pro	Thr	Glu	Ala	Asn	Pro	Lys	Thr	Glu	Gln	Pro	Thr
				165					170					175	
Ile	Pro	Ile	Ser	Arg	Glu	Phe	Glu	Glu	Phe	Cys	Ala	Lys	His	Glu	Ala
			180					185					190		
Glu	Gln	Gln	Arg	Glu	Phe	Met	Glu	Lys	Tyr	Asn	Phe	Asp	Pro	Val	Thr
	195						200				205				
Glu	Gln	Pro	Leu	Pro	Gly	Arg	Tyr	Glu	Trp	Glu	Lys	Val	Ser	Pro	
	210					215					220				

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe or
 Primer

<400> 7
 cgagatctga attcatggat cagta 25

<210> 8
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe or
 Primer

<400> 8
 cgagatctga attcctaagg catgcc 26

<210> 9
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe or
 Primer

<400> 9
 gggaatccat gggcggcggt taggagaag 29

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 10
ggcggatccc gtcttcttca tggattc

27

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 11
ggcgaatcca tggaagtctc taaagcaac

29

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 12
ggcggatcct tttgaacttc atggtttgac

30

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 13
cggctcgagg agaaccacaa acacgc

26

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 14
cgaaactagt taattacctc aaggaag 27

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 15
gatcccgggc gatatcagcg tcatgg 26

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 16
gatcccgggt tagtctgtta actcc 25

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 17
gcagctacgg agccggagaa ttgt 24

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 18
tctccttctc gaaatcgaaa ttgtact

27

<210> 19
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 19
cggctcgagg agaaccacaa acacgc

26

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 20
cgaaactagt taattacctc aaggaag

27

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 21
gatcccgggc gatatcagcg tcatgg

26

<210> 22
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 22
gatcccggt tagtctgtta actcc

25

<210> 23
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 23
cccgctcgag atggtgagaa aatatagaaa agctaaagga tttgtagaag ctggagtttc 60
gtcaacgta 69

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 24
ggactagttc actctaactt taccattcg

30

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 25
gatcatctta agcatcatcg tcttcttcat gg

32

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 26

taggagcata tggcggcgg

19

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 27

atatcagcgc catggaagtc

20

<210> 28

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 28

ggagctggat ccttttggaa ttcattg

27

<210> 29

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 29

taggagcata tggcggcgg

19

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe or
Primer

<400> 30

atcatcgaat tcttcattgga ttc

23

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 31
atatcagcgc catggaagtc 20

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe or
Primer

<400> 32
ggagctggat ccttttggaa ttcattgg 27

<210> 33
<211> 11
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (5)
<223> Xaa at position 5 may be Asp or Glu

<220>
<221> UNSURE
<222> (6)..(8)
<223> Xaa at any of positions 6, 7 or 8 may be any amino
acid

<400> 33
Val Arg Arg Arg Xaa Xaa Xaa Val Glu Glu
1 5 10

<210> 34
<211> 8
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)..(3)
<223> Xaa at positions 2 and 3 may be any amino acid

<400> 34
Phe Xaa Xaa Lys Tyr Asn Phe Asp
1 5

<210> 35
<211> 8
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (1)
<223> Xaa at position 1 may be Pro or Leu

<220>
<221> UNSURE
<222> (3)
<223> Xaa at position 3 may be any amino acid

<400> 35
Xaa Leu Xaa Gly Arg Tyr Glu Trp
1 5

<210> 36
<211> 10
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid

<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 may be Asp or Glu

<220>
<221> UNSURE
<222> (7)..(9)
<223> Xaa at positions 7, 8 or 9 may be any amino acid

<400> 36
Glu Xaa Glu Xaa Phe Phe Xaa Xaa Xaa Glu
1 5 10

<210> 37
<211> 8
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid

<400> 37
Tyr Xaa Gln Leu Arg Ser Arg Arg
1 5

<210> 38
 <211> 9
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> UNSURE
 <222> (5)
 <223> Xaa at position 5 may be Met or Ile

<220>
 <221> UNSURE
 <222> (6)
 <223> Xaa at position 6 may be Lys or Arg

<220>
 <221> UNSURE
 <222> (8)
 <223> Xaa at position 8 may be any amino acid

<220>
 <221> UNSURE
 <222> (9)
 <223> Xaa at position 9 may be Lys or Arg

<400> 38
 Met Gly Lys Tyr Xaa Xaa Lys Xaa Xaa
 1 5

<210> 39
 <211> 8
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> UNSURE
 <222> (2)
 <223> Xaa at position 2 may be any amino acid

<400> 39
 Ser Xaa Gly Val Arg Thr Arg Ala
 1 5

<210> 40
 <211> 327
 <212> PRT
 <213> Arabidopsis thaliana

<400> 40
 Met Gly Lys Tyr Ile Arg Lys Ser Lys Ile Asp Gly Ala Gly Ala Gly
 1 5 10 15
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ser Ser Ile Ala
 20 25 30
 Leu Met Asp Val Val Ser Pro Ser Ser Ser Ser Ser Leu Gly Val Leu
 35 40 45
 Thr Arg Ala Lys Ser Leu Ala Leu Gln Gln Gln Gln Gln Arg Cys Leu
 50 55 60

Leu 65	Gln	Lys	Pro	Ser	Ser 70	Pro	Ser	Ser	Leu	Pro 75	Pro	Thr	Ser	Ala	Ser 80
Pro	Asn	Pro	Pro	Ser 85	Lys	Gln	Lys	Met	Lys 90	Lys	Lys	Gln	Gln	Gln	Met
Asn	Asp	Cys	Gly 100	Ser	Tyr	Leu	Gln	Leu 105	Arg	Ser	Arg	Arg	Leu 110	Gln	Lys
Lys	Pro	Pro	Ile 115	Val	Val	Ile	Arg	Ser 120	Thr	Lys	Arg	Arg	Lys 125	Gln	Gln
Arg	Arg 130	Asn	Glu	Thr	Cys	Gly 135	Arg	Asn	Pro	Asn	Pro 140	Arg	Ser	Asn	Leu
Asp 145	Ser	Ile	Arg	Gly	Asp 150	Gly	Ser	Arg	Ser	Asp 155	Ser	Val	Ser	Glu	Ser 160
Val	Val	Phe	Gly 165	Lys	Asp	Lys	Asp	Leu	Ile 170	Ser	Glu	Ile	Asn	Lys 175	Asp
Pro	Thr	Phe	Gly 180	Gln	Asn	Phe	Phe	Asp 185	Leu	Glu	Glu	Glu	His 190	Thr	Gln
Ser	Phe	Asn 195	Arg	Thr	Thr	Arg	Glu 200	Ser	Thr	Pro	Cys	Ser 205	Leu	Ile	Arg
Arg	Pro 210	Glu	Ile	Met	Thr	Thr 215	Pro	Gly	Ser	Ser 220	Thr	Lys	Leu	Asn	Ile
Cys 225	Val	Ser	Glu	Ser	Asn 230	Gln	Arg	Glu	Asp 235	Ser	Leu	Ser	Arg	Ser	His 240
Arg	Arg	Arg	Pro 245	Thr	Thr	Pro	Glu	Met	Asp 250	Glu	Phe	Phe	Ser	Gly	Ala
Glu	Glu	Glu	Gln 260	Lys	Gln	Phe	Ile 265	Glu	Lys	Tyr	Val	Phe 270	Val	Pro	Arg
Phe	Ile	Cys 275	Ser	Val	Leu	Leu 280	Val	Met	Ser	Phe	Gln 285	Phe	Val	Leu	Phe
Phe	Ser	Phe 290	Gly	Leu	Val	Ser 295	Leu	Met	Val	Ser 300	Val	Asn	Ser	Phe	Phe
Arg 305	Tyr	Asn	Phe	Asp 310	Pro	Val	Asn	Glu	Gln 315	Pro	Leu	Pro	Gly	Arg	Phe 320
Glu	Trp	Thr	Lys 325	Val	Asp	Asp									

```
<210> 41
<211> 22
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Probe or
Primer

```
<400> 41
agaccatggc ggcggttagg ag
```

22

```
<210> 42
<211> 12
<212> PRT
<213> Tag·100 epitope
```

<400> 42
Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser
1 5 10

<210> 43
<211> 10
<212> PRT
<213> c-myc epitope

<400> 43
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 44
<211> 7
<212> PRT
<213> FLAG-epitope

<400> 44
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 45
<211> 9
<212> PRT
<213> HA-epitope

<400> 45
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 46
<211> 12
<212> PRT
<213> protein C epitope

<400> 46
Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

<210> 47
<211> 11
<212> PRT
<213> VSV epitope

<400> 47
Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
1 5 10

<210> 48
<211> 9
<212> DNA
<213> Escherichia coli

<400> 48
agg aga aga
Arg Arg Arg
1